SEQUENCE LISTING

<110> NISHIO, FUMIHIDE

<120> HIGH-CONCENTRATION PREPARATION OF SOLUBLE THROMBOMODULIN

<130> 8062-1023

<140> 10/501,671
<141> 2004-07-16

<150> PCT/JP03/00339
<151> 2003-01-17

<150> JP2002-9951
<151> 2002-01-18

<160> 9

<170> PatentIn Ver. 3.3

<210> 1
<211> 516
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Partial amino acid sequence of human-originated soluble thrombomodulin

<400> 1

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Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
  1               5                  10                  15

Phe Pro Ala Pro Ala Glu Pro Gln Pro Gly Gly Ser Gln Cys Val Glu
            20                  25                  30

His Asp Cys Phe Ala Leu Tyr Pro Gly Pro Ala Thr Phe Leu Asn Ala
        35                  40                  45

Ser Gln Ile Cys Asp Gly Leu Arg Gly His Leu Met Thr Val Arg Ser
    50                  55                  60

Ser Val Ala Ala Asp Val Ile Ser Leu Leu Leu Asn Gly Asp Gly Gly
65                  70                  75                  80

Val Gly Arg Arg Arg Leu Trp Ile Gly Leu Gln Leu Pro Pro Gly Cys
                85                  90                  95

Gly Asp Pro Lys Arg Leu Gly Pro Leu Arg Gly Phe Gln Trp Val Thr
            100                 105                 110

Gly Asp Asn Asn Thr Ser Tyr Ser Arg Trp Ala Arg Leu Asp Leu Asn
        115                 120                 125
```

```
Gly Ala Pro Leu Cys Gly Pro Leu Cys Val Ala Val Ser Ala Ala Glu
    130                 135                 140

Ala Thr Val Pro Ser Glu Pro Ile Trp Glu Glu Gln Gln Cys Glu Val
145                 150                 155                 160

Lys Ala Asp Gly Phe Leu Cys Glu Phe His Phe Pro Ala Thr Cys Arg
                165                 170                 175

Pro Leu Ala Val Glu Pro Gly Ala Ala Ala Ala Val Ser Ile Thr
            180                 185                 190

Tyr Gly Thr Pro Phe Ala Ala Arg Gly Ala Asp Phe Gln Ala Leu Pro
        195                 200                 205

Val Gly Ser Ser Ala Ala Val Ala Pro Leu Gly Leu Gln Leu Met Cys
    210                 215                 220

Thr Ala Pro Pro Gly Ala Val Gln Gly His Trp Ala Arg Glu Ala Pro
225                 230                 235                 240

Gly Ala Trp Asp Cys Ser Val Glu Asn Gly Gly Cys Glu His Ala Cys
                245                 250                 255

Asn Ala Ile Pro Gly Ala Pro Arg Cys Gln Cys Pro Ala Gly Ala Ala
            260                 265                 270

Leu Gln Ala Asp Gly Arg Ser Cys Thr Ala Ser Ala Thr Gln Ser Cys
        275                 280                 285

Asn Asp Leu Cys Glu His Phe Cys Val Pro Asn Pro Asp Gln Pro Gly
    290                 295                 300

Ser Tyr Ser Cys Met Cys Glu Thr Gly Tyr Arg Leu Ala Ala Asp Gln
305                 310                 315                 320

His Arg Cys Glu Asp Val Asp Asp Cys Ile Leu Glu Pro Ser Pro Cys
                325                 330                 335

Pro Gln Arg Cys Val Asn Thr Gln Gly Gly Phe Glu Cys His Cys Tyr
            340                 345                 350

Pro Asn Tyr Asp Leu Val Asp Gly Glu Cys Val Glu Pro Val Asp Pro
        355                 360                 365

Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro Leu Asn Gln Thr
    370                 375                 380

Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro Ile Pro His Glu
385                 390                 395                 400

Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala Cys Pro Ala Asp
                405                 410                 415

Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro Glu Gly Tyr Ile
            420                 425                 430
```

```
Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu Cys Glu Asn Gly
        435                 440                 445

Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly Thr Phe Glu Cys
    450                 455                 460

Ile Cys Gly Pro Asp Ser Ala Leu Val Arg His Ile Gly Thr Asp Cys
465                 470                 475                 480

Asp Ser Gly Lys Val Asp Gly Gly Asp Ser Gly Ser Gly Glu Pro Pro
                485                 490                 495

Pro Ser Pro Thr Pro Gly Ser Thr Leu Thr Pro Pro Ala Val Gly Leu
            500                 505                 510

Val His Ser Gly
        515
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<210> 2
<211> 1548
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Partial base sequence of human-originated soluble thrombomodulin gene

<400> 2

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gcagagccgc agccgggtgg cagccagtgc gtcgagcacg actgcttcgc gctctacccg 120
ggccccgcga ccttcctcaa tgccagtcag atctgcgacg gactgcgggg ccacctaatg 180
acagtgcgct cctcggtggc tgccgatgtc atttccttgc tactgaacgg cgacggcggc 240
gttggccgcc ggcgcctctg gatcggcctg cagctgccac ccggctgcgg cgaccccaag 300
cgcctcgggc ccctgcgcgg cttccagtgg gttacgggag acaacaacac cagctatagc 360
aggtgggcac ggctcgacct caatggggct cccctctgcg gcccgttgtg cgtcgctgtc 420
tccgctgctg aggccactgt gcccagcgag ccgatctggg aggagcagca gtgcgaagtg 480
aaggccgatg gcttcctctg cgagttccac ttcccagcca cctgcaggcc actggctgtg 540
gagcccggcg ccgcggctgc cgccgtctcg atcacctacg gcaccccgtt cgcggcccgc 600
ggagcggact tccaggcgct gccggtgggc agctccgccg cggtggctcc cctcggctta 660
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ggcgcttggg actgcagcgt ggagaacggc ggctgcgagc acgcgtgcaa tgcgatccct 780
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gaccagccgg gctcctactc gtgcatgtgc gagaccggct accggctggc ggccgaccaa 960
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ctgaaccaaa ctagctacct ctgcgtctgc gccgagggct tcgcgcccat tccccacgag 1200
ccgcacaggt gccagatgtt ttgcaaccag actgcctgtc cagccgactg cgaccccaac 1260
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accttcgagt gcatctgcgg gcccgactcg gcccttgtcc gccacattgg caccgactgt 1440
gactccggca aggtggacgg tggcgacagc ggctctggcg agcccccgcc cagcccgacg 1500
cccggctcca ccttgactcc tccggccgtg gggctcgtgc attcgggc               1548
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<210> 3
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Partial amino acid sequence of human-originated soluble thrombomodulin

<400> 3

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Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
  1               5                  10                  15

Phe Pro Asp Pro Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro
             20                  25                  30

Leu Asn Gln Thr Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro
         35                  40                  45

Ile Pro His Glu Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala
     50                  55                  60

Cys Pro Ala Asp Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro
 65                  70                  75                  80

Glu Gly Tyr Ile Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu
                 85                  90                  95

Cys Glu Asn Gly Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly
            100                 105                 110

Thr Phe Glu Cys Ile Cys Gly Pro Asp Ser Ala Leu Val Arg His Ile
        115                 120                 125

Gly Thr Asp Cys
    130
```

<210> 4
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Partial base sequence of human-originated soluble thrombomodulin gene

<400> 4

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atgcttgggg tcctggtcct tggcgcgctg gccctggccg gcctggggtt ccccgacccg 60
tgcttcagag ccaactgcga gtaccagtgc cagcccctga accaaactag ctacctctgc 120
gtctgcgccg agggcttcgc gcccattccc cacgagccgc acaggtgcca gatgttttgc 180
aaccagactg cctgtccagc cgactgcgac cccaacaccc aggctagctg tgagtgccct 240
gaaggctaca tcctggacga cggtttcatc tgcacggaca tcgacgagtg cgaaaacggc 300
ggcttctgct ccggggtgtg ccacaacctc cccggtacct tcgagtgcat ctgcgggccc 360
gactcggccc ttgtccgcca cattggcacc gactgt                           396
```

<210> 5
<211> 516
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Partial amino acid sequence of human-originated soluble thrombomodulin

<400> 5

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Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
  1               5                  10                  15

Phe Pro Ala Pro Ala Glu Pro Gln Pro Gly Gly Ser Gln Cys Val Glu
             20                  25                  30

His Asp Cys Phe Ala Leu Tyr Pro Gly Pro Ala Thr Phe Leu Asn Ala
         35                  40                  45

Ser Gln Ile Cys Asp Gly Leu Arg Gly His Leu Met Thr Val Arg Ser
     50                  55                  60

Ser Val Ala Ala Asp Val Ile Ser Leu Leu Leu Asn Gly Asp Gly Gly
 65                  70                  75                  80

Val Gly Arg Arg Arg Leu Trp Ile Gly Leu Gln Leu Pro Pro Gly Cys
                 85                  90                  95

Gly Asp Pro Lys Arg Leu Gly Pro Leu Arg Gly Phe Gln Trp Val Thr
            100                 105                 110

Gly Asp Asn Asn Thr Ser Tyr Ser Arg Trp Ala Arg Leu Asp Leu Asn
        115                 120                 125

Gly Ala Pro Leu Cys Gly Pro Leu Cys Val Ala Val Ser Ala Ala Glu
    130                 135                 140

Ala Thr Val Pro Ser Glu Pro Ile Trp Glu Glu Gln Gln Cys Glu Val
145                 150                 155                 160

Lys Ala Asp Gly Phe Leu Cys Glu Phe His Phe Pro Ala Thr Cys Arg
                165                 170                 175

Pro Leu Ala Val Glu Pro Gly Ala Ala Ala Ala Ala Val Ser Ile Thr
            180                 185                 190

Tyr Gly Thr Pro Phe Ala Ala Arg Gly Ala Asp Phe Gln Ala Leu Pro
        195                 200                 205

Val Gly Ser Ser Ala Ala Val Ala Pro Leu Gly Leu Gln Leu Met Cys
    210                 215                 220

Thr Ala Pro Pro Gly Ala Val Gln Gly His Trp Ala Arg Glu Ala Pro
225                 230                 235                 240
```

```
Gly Ala Trp Asp Cys Ser Val Glu Asn Gly Gly Cys Glu His Ala Cys
                245                 250                 255

Asn Ala Ile Pro Gly Ala Pro Arg Cys Gln Cys Pro Ala Gly Ala Ala
            260                 265                 270

Leu Gln Ala Asp Gly Arg Ser Cys Thr Ala Ser Ala Thr Gln Ser Cys
        275                 280                 285

Asn Asp Leu Cys Glu His Phe Cys Val Pro Asn Pro Asp Gln Pro Gly
    290                 295                 300

Ser Tyr Ser Cys Met Cys Glu Thr Gly Tyr Arg Leu Ala Ala Asp Gln
305                 310                 315                 320

His Arg Cys Glu Asp Val Asp Asp Cys Ile Leu Glu Pro Ser Pro Cys
                325                 330                 335

Pro Gln Arg Cys Val Asn Thr Gln Gly Gly Phe Glu Cys His Cys Tyr
            340                 345                 350

Pro Asn Tyr Asp Leu Val Asp Gly Glu Cys Val Glu Pro Val Asp Pro
        355                 360                 365

Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro Leu Asn Gln Thr
    370                 375                 380

Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro Ile Pro His Glu
385                 390                 395                 400

Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala Cys Pro Ala Asp
                405                 410                 415

Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro Glu Gly Tyr Ile
            420                 425                 430

Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu Cys Glu Asn Gly
        435                 440                 445

Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly Thr Phe Glu Cys
    450                 455                 460

Ile Cys Gly Pro Asp Ser Ala Leu Ala Arg His Ile Gly Thr Asp Cys
465                 470                 475                 480

Asp Ser Gly Lys Val Asp Gly Gly Asp Ser Gly Ser Gly Glu Pro Pro
                485                 490                 495

Pro Ser Pro Thr Pro Gly Ser Thr Leu Thr Pro Pro Ala Val Gly Leu
            500                 505                 510

Val His Ser Gly
        515
```

<210> 6
<211> 1548
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Partial base sequence of human-originated soluble thrombomodulin gene

<400> 6
atgcttgggg tcctggtcct tggcgcgctg gccctggccg gcctggggtt ccccgcaccc 60
gcagagccgc agccgggtgg cagccagtgc gtcgagcacg actgcttcgc gctctacccg 120
ggccccgcga ccttcctcaa tgccagtcag atctgcgacg gactgcgggg ccacctaatg 180
acagtgcgct cctcggtggc tgccgatgtc atttccttgc tactgaacgg cgacggcggc 240
gttggccgcc ggcgcctctg gatcggcctg cagctgccac ccggctgcgg cgaccccaag 300
cgcctcgggc ccctgcgcgg cttccagtgg gttacgggag acaacaacac cagctatagc 360
aggtgggcac ggctcgacct caatggggct cccctctgcg gcccgttgtg cgtcgctgtc 420
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aaggccgatg gcttcctctg cgagttccac ttcccagcca cctgcaggcc actggctgtg 540
gagcccggcg ccgcggctgc cgccgtctcg atcacctacg gcaccccgtt cgcggcccgc 600
ggagcggact tccaggcgct gccggtgggc agctccgccg cggtggctcc cctcggctta 660
cagctaatgt gcaccgcgcc gcccggagcg gtccaggggc actgggccag ggaggcgccg 720
ggcgcttggg actgcagcgt ggagaacggc ggctgcgagc acgcgtgcaa tgcgatccct 780
ggggctcccc gctgccagtg cccagccggc gccgccctgc aggcagacgg gcgctcctgc 840
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gaccagccgg gctcctactc gtgcatgtgc gagaccggct accggctggc ggccgaccaa 960
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gagtgtgtgg agcccgtgga cccgtgcttc agagccaact gcgagtacca gtgccagccc 1140
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ccgcacaggt gccagatgtt ttgcaaccag actgcctgtc cagccgactg cgaccccaac 1260
acccaggcta gctgtgagtg ccctgaaggc tacatcctgg acgacggttt catctgcacg 1320
gacatcgacg agtgcgaaaa cggcggcttc tgctccgggg tgtgccacaa cctccccggt 1380
accttcgagt gcatctgcgg gcccgactcg gcccttgccc gccacattgg caccgactgt 1440
gactccggca aggtggacgg tggcgacagc ggctctggcg agcccccgcc cagcccgacg 1500
cccggctcca ccttgactcc tccggccgtg gggctcgtgc attcgggc 1548

<210> 7
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Partial amino acid sequence of human-originated soluble thrombomodulin

<400> 7
Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
1 5 10 15

Phe Pro Asp Pro Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro
20 25 30

Leu Asn Gln Thr Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro
35 40 45

```
Ile Pro His Glu Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala
 50                  55                  60

Cys Pro Ala Asp Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro
65                  70                  75                  80

Glu Gly Tyr Ile Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu
                85                  90                  95

Cys Glu Asn Gly Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly
            100                 105                 110

Thr Phe Glu Cys Ile Cys Gly Pro Asp Ser Ala Leu Ala Arg His Ile
        115                 120                 125

Gly Thr Asp Cys
    130
```

<210> 8
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Partial base sequence of human-originated soluble thrombomodulin gene

<400> 8
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tgcttcagag ccaactgcga gtaccagtgc cagcccctga accaaactag ctacctctgc 120
gtctgcgccg agggcttcgc gcccattccc cacgagccgc acaggtgcca gatgttttgc 180
aäccagactg cctgtccagc cgactgcgac cccaacaccc aggctagctg tgagtgccct 240
gaaggctaca tcctggacga cggtttcatc tgcacggaca tcgacgagtg cgaaaacggc 300
ggcttctgct ccggggtgtg ccacaacctc cccggtacct tcgagtgcat ctgcgggccc 360
gactcggccc ttgcccgcca cattggcacc gactgt 396

<210> 9
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA for mutation

<400> 9
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